

## SEQUENCE LISTING

<110> Crucell Holland B.V.

Bakker, Alexander B.H.

Meester-Rood, Pauline M.L.

Bakker, Adrianus Q.

<120> AGONISTIC BINDING MOLECULES TO THE HUMAN OX40 RECEPTOR

<130> 0077 WO 00 ORD

<150> PCT/NL02/00389

<151> 2002-06-13

<160> 54

<170> PatentIn version 3.1

<210> 1

<211> 769

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02008

<220>

<221> CDS

<222> (3)..(767)

<223>

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47

cct gga ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt  
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
20 25 30

95

agc aac tac acg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg Ser Asn Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 35 40 45	143
gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala 50 55 60	191
gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn 65 70 75	239
acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val 80 85 90 95	287
tat tac tgt gcc aaa gac cgc tac tcc cag gtg cac tac gcg ttg gat Tyr Tyr Cys Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp 100 105 110	335
tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly 115 120 125	383
tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac atc cag Ser Gly Gly Thr Gly Ser Gly Thr Gly Ser Glu Leu Asp Ile Gln 130 135 140	431
atg acg cag tct cca gac tca ctg ccc gtc acc cct gga gag ccg gcc Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro Ala 145 150 155	479
tcc atc tcc tgc agg tct agt cag agc ctc ctg cat agt aat gga tac Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr 160 165 170 175	527
aac tat ttg gat tgg tac ctg cag aag gca ggg cag tct cca cag ctc Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser Pro Gln Leu 180 185 190	575
ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe 195 200 205	623
agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val 210 215 220	671
gag gct gag gat gtt ggg gtt tat tac tgc cag cag tac tac aac cac Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn His 225 230 235	719
ccg acg acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc gcg gcc Pro Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala 240 245 250 255	767
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<213> Artificial sequence	

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&lt;223&gt; scFv SC02008

&lt;400&gt; 2

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1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser  
20 25 30

Asn Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp  
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
85 90 95

Tyr Cys Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp Tyr  
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser  
115 120 125

Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met  
130 135 140

Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser  
145 150 155 160

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn  
165 170 175

Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser Pro Gln Leu Leu  
180 185 190

Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser  
195 200 205

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu  
210 215 220

Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn His Pro  
225 230 235 240

Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala  
 245 250 255

<210> 3

<211> 775

<212> DNA

<213> Artificial sequence

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<223> scFv SC02009

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<221> CDS

<222> (3)...(773)

<223>

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 1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 95  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 20 25 30

agc ggc tac tct atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg 143  
 Ser Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 35 40 45

gag tgg gtt ggc cgt act aga aac aaa gct aac agt tac acc aca gaa 191  
 Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu  
 50 55 60

tac gcc gcg tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca 239  
 Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser  
 65 70 75

aag aac tca ctg tat ctg caa atg aac agt ctg aga gcc gag gac aca 287  
 Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr  
 80 85 90 95

gcc gtg tat tac tgt gcc aaa gac cgc tac gtc aac acg tcg aac gcg 335  
 Ala Val Tyr Tyr Cys Ala Lys Asp Arg Tyr Val Asn Thr Ser Asn Ala  
 100 105 110

ttc gat tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc 383  
 Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr  
 115 120 125

gga ggt tcc ggc gga acc ggg tct ggg act ggt acg acg gag ctc gac 431  
 Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp  
 130 135 140

atc cag atg aca cag tct cca gac tca ctg ccc gtc acc cct gga gag 479  
 Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu  
 145 150 155

ccg gcc tcc atc tcc tgc aga tct agt cag agc ctc ctg cat agt aat	527
Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn	
160 165 170 175	
gga tac aac tat ttg gat tgg tac ctg cag aag cca ggg cag tct cca	575
Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro	
180 185 190	
cag ctc ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac	623
Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp	
195 200 205	
agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc	671
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser	
210 215 220	
aga gtg gag gct cac cat gtt ggg gtt tat tac tgc cag cag tac ccg	719
Arg Val Glu Ala His His Val Gly Val Tyr Tyr Cys Gln Gln Tyr Pro	
225 230 235	
ctg ggc ccc acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc	767
Leu Gly Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg	
240 245 250 255	
gcg gcc gc	775
Ala Ala	

&lt;210&gt; 4

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; scFv SC02009

&lt;400&gt; 4

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Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser	
20 25 30	

Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu	
35 40 45	

Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr	
50 55 60	

Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys	
65 70 75 80	

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala	
85 90 95	

Val Tyr Tyr Cys Ala Lys Asp Arg Tyr Val Asn Thr Ser Asn Ala Phe  
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly  
115 120 125

Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile  
130 135 140

Gln Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro  
145 150 155 160

Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly  
165 170 175

Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln  
180 185 190

Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg  
195 200 205

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg  
210 215 220

Val Glu Ala His His Val Gly Val Tyr Tyr Cys Gln Gln Tyr Pro Leu  
225 230 235 240

Gly Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala  
245 250 255

Ala

<210> 5

<211> 736

<212> DNA

<213> Artificial sequence

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<222> (3)...(734)

<223>

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 1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 95  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 20 25 30

agc ggc tac cct atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg 143  
 Ser Gly Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 35 40 45

gag tgg gtg gca gtt ata tca tat gat gga agt aat aaa tac tac gca 191  
 Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala  
 50 55 60

gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac 239  
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn  
 65 70 75

acg ctg tat ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg 287  
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
 80 85 90 95

tat tac tgt gca aga gac atg tcc ggc ttc cac gag ttc gat tac tgg 335  
 Tyr Tyr Cys Ala Arg Asp Met Ser Gly Phe His Glu Phe Asp Tyr Trp  
 100 105 110

ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc 383  
 Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly  
 115 120 125

gga acc ggg tct ggg act ggt acg agc gag ctc acc cag tct cca tcc 431  
 Gly Thr Gly Ser Gly Thr Gly Ser Glu Leu Thr Gln Ser Pro Ser  
 130 135 140

tcc ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca 479  
 Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala  
 145 150 155

agt cag agc att agc agc tac tta aat tgg tat cag cag aaa cca ggg 527  
 Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly  
 160 165 170 175

aaa gcc cct aag ctc ctg atc tat gct gca tcc agt ttg caa agt ggg 575  
 Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly  
 180 185 190

gtc cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc 623  
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
 195 200 205

acc atc agc agt ctg caa cct gaa gat ttt gca act tac tac tgt caa 671  
 Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln  
 210 215 220

cag agt tac agt acc cct cca acg ttc ggc caa ggg acc aag gtg gag 719  
 Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu  
 225 230 235

atc aaa cgt gcg gcc gc 736  
 Ile Lys Arg Ala Ala  
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<210> 6  
<211> 244  
<212> PRT  
<213> Artificial sequence

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&lt;223&gt; scFv SC02010

&lt;400&gt; 6

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20 25 30

Gly Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp  
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
85 90 95

Tyr Cys Ala Arg Asp Met Ser Gly Phe His Glu Phe Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly  
115 120 125

Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser Ser  
130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
145 150 155 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys  
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val  
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
 210 215 220

Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
 225 230 235 240

Lys Arg Ala Ala

<210> 7

<211> 763

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02011

<220>

<221> CDS

<222> (3)..(761)

<223>

<400> 7

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 1 5 10 15

cct ggg agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 95  
 Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 20 25 30

agc gac tac acg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg 143  
 Ser Asp Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 35 40 45

gag tgg gtc tca tcc att agt ggt agc aca tac tac gca gac tcc 191  
 Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser  
 50 55 60

agg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg 239  
 Arg Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu  
 65 70 75

tat ctt caa atg aac aac ctg aga gct gag gac acg gcc gtg tat tac 287  
 Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr  
 80 85 90 95

tgt gca aga gac cgc tac ttc agg cag cag aac ggc ttc gat tac tgg 335  
 Cys Ala Arg Asp Arg Tyr Phe Arg Gln Gln Asn Ala Phe Asp Tyr Trp  
 100 105 110

ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc 383  
 Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly  
 115 120 125

gga acc ggg tct ggg act ggt acg acg gag ctc gac atc cag atg act	431
Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met Thr	
130 135 140	
cag tct cca gtc acc ctg ccc gtc acc cct gga gag ccg gcc tcc atc	479
Gln Ser Pro Val Thr Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile	
145 150 155	
tcc tgc agg tct agt cag agc ctc ctg cat agt aat gga tac aac tat	527
Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr	
160 165 170 175	
ttg gat tgg tac ctg cag aag cca ggg cag tct cca cag ctc ctg atc	575
Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile	
180 185 190	
tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc agt ggc	623
Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly	
195 200 205	
agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg gag gct	671
Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala	
210 215 220	
gag gat gtt ggg gtt tat tac tgc cag cag tac ctc acg gcc ccg ccc	719
Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Leu Thr Ala Pro Pro	
225 230 235	
acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc gcg gcc gc	763
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala	
240 245 250	
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20 25 30	
Asp Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu	
35 40 45	
Trp Val Ser Ser Ile Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Arg	
50 55 60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	

Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Arg Tyr Phe Arg Gln Gln Asn Ala Phe Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly  
115 120 125

Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met Thr Gln  
130 135 140

Ser Pro Val Thr Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser  
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu  
165 170 175

Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr  
180 185 190

Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu  
210 215 220

Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Leu Thr Ala Pro Pro Thr  
225 230 235 240

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala  
245 250

<210> 9

<211> 748

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02012

<220>

<221> CDS

<222> (3)...(746)

<223>

<400> 9

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1 5 10 15	
ccg ggt ggc agc ctg cgc ctg agc tgc gcc gct agc ggc ttc acc ttt	95
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
20 25 30	
agc aac gac tcg atg aac tgg atg cgc cag gcc ccc ggc aaa ggc ctc	143
Ser Asn Asp Ser Met Asn Trp Met Arg Gln Ala Pro Gly Lys Gly Leu	
35 40 45	
gaa tgg gtt gcc aat atc aat cag gat ggc aac gaa aaa tat tac gcc	191
Glu Trp Val Ala Asn Ile Asn Gln Asp Gly Asn Glu Lys Tyr Tyr Ala	
50 55 60	
gac tct gtc aaa ggc cgc ttc acc atc agt cgc gat aac tcc aaa aac	239
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn	
65 70 75	
tcc ctg tac ctg cag atg aac agc ctg cgc gac gaa gat acc gcc ctg	287
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Leu	
80 85 90 95	
tac tac tgc gca cgc gcc cgc gcc ggc acc atc ttc gat tac tgg	335
Tyr Tyr Cys Ala Arg Ala Ala Gly Thr Ile Phe Asp Tyr Trp	
100 105 110	
ggc cag ggc acc ctg gtt acc gtc ctc gag ggt acc gga ggt tcc ggc	383
Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly	
115 120 125	
gga acc ggg tct ggg act ggt acg agc gag ctc gat atc cag atg acc	431
Gly Thr Gly Ser Gly Thr Gly Ser Glu Leu Asp Ile Gln Met Thr	
130 135 140	
cag agc ccg agt tcc ctg agc gcc tcc gtt ggc gac cgc gtt acc atc	479
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile	
145 150 155	
acc tgc cgc gcc agc cag aac gtc agc aac tac ctg acc tgg tac cag	527
Thr Cys Arg Ala Ser Gln Asn Val Ser Asn Tyr Leu Thr Trp Tyr Gln	
160 165 170 175	
cag aaa ccg ggc aag gct ggc aaa ctg ctg att tac gcc gcc agc agc	575
Gln Lys Pro Gly Lys Ala Gly Lys Leu Leu Ile Tyr Ala Ala Ser Ser	
180 185 190	
ctc caa agc ggc gtt ccg tct aga ttc agt ggc tcc ggc tcc gga acc	623
Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr	
195 200 205	
gat ttt acc ctg acc atc agc agc ctg cag ccg gaa gat ttc gct acc	671
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr	
210 215 220	
tac tat tgt cag cag tcc tac ttc aac ccg gcg acc ttc ggc cag ggc	719
Tyr Tyr Cys Gln Gln Ser Tyr Phe Asn Pro Ala Thr Phe Gly Gln Gly	
225 230 235	
acc aaa ctg gaa atc aaa cgc gcg gcc gc	748
Thr Lys Leu Glu Ile Lys Arg Ala Ala	
240 245	

&lt;210&gt; 10

&lt;211&gt; 248

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; scFv SC02012

&lt;400&gt; 10

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro  
1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser  
20 25 30

Asn Asp Ser Met Asn Trp Met Arg Gln Ala Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Val Ala Asn Ile Asn Gln Asp Gly Asn Glu Lys Tyr Tyr Ala Asp  
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Leu Tyr  
85 90 95

Tyr Cys Ala Arg Ala Arg Ala Ala Gly Thr Ile Phe Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly  
115 120 125

Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met Thr Gln  
130 135 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr  
145 150 155 160

Cys Arg Ala Ser Gln Asn Val Ser Asn Tyr Leu Thr Trp Tyr Gln Gln  
165 170 175

Lys Pro Gly Lys Ala Gly Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu  
180 185 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
195 200 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr  
 210 215 220

Tyr Cys Gln Gln Ser Tyr Phe Asn Pro Ala Thr Phe Gly Gln Gly Thr  
 225 230 235 240

Lys Leu Glu Ile Lys Arg Ala Ala  
 245

<210> 11

<211> 769

<212> DNA

<213> Artificial sequence

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<223> scFv SC02021

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<221> CDS

<222> (3) .. (767)

<223>

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Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln	
1 5 10 15	

cct agg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt	95
Pro Arg Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
20 25 30	

agc agc tac gcg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg	143
Ser Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
35 40 45	

gag tgg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac gca	191
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala	
50 55 60	

gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac	239
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn	
65 70 75	

acg ctg tat ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg	287
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val	
80 85 90 95	

tat tac tgt gcc aaa gac cgc tac atc acg ttg ccg aac gcg ttg gat	335
Tyr Tyr Cys Ala Lys Asp Arg Tyr Ile Thr Leu Pro Asn Ala Leu Asp	
100 105 110	

tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt	383
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly	
115 120 125	

tcc ggc gga acc ggg tct ggg act ggt acg acg gag ctc gac atc cag Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln 130 135 140	431
atg acc cag tct cca gtc tca ctg ccc gtc acc cct gga gag ccg gcc Met Thr Gln Ser Pro Val Ser Leu Pro Val Thr Pro Gly Glu Pro Ala 145 150 155	479
tcc atc tcc tgc agg tct agt cag agc ctc ctg cat agt aat gga tac Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr 160 165 170 175	527
aac tat ttg gat tgg tac ctg cag aag cca ggg cag tct cca cag ctc Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu 180 185 190	575
ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe 195 200 205	623
agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val 210 215 220	671
gag gct gag gat gtt ggg gtt tat tac tgc cag cag tac aag tcg aac Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Lys Ser Asn 225 230 235	719
ccg ccc acc ttc ggc cag ggc acc aaa gtg gaa atc aaa cgcc ggc Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala 240 245 250 255	767
gc	769
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<211> 255	
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<400> 12	
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro 1 5 10 15	
Arg Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser 20 25 30	
Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu 35 40 45	
Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp 50 55 60	

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
85 90 95

Tyr Cys Ala Lys Asp Arg Tyr Ile Thr Leu Pro Asn Ala Leu Asp Tyr  
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser  
115 120 125

Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met  
130 135 140

Thr Gln Ser Pro Val Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser  
145 150 155 160

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn  
165 170 175

Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu  
180 185 190

Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser  
195 200 205

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu  
210 215 220

Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Lys Ser Asn Pro  
225 230 235 240

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala  
245 250 255

<210> 13

<211> 745

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02022

<220>

<221> CDS

<222> (3) .. (743)

&lt;223&gt;

<400> 13  
 cc atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cat 47  
 Met Ala Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His  
 1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc 95  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe  
 20 25 30

agt agc tat gct atg cac tgg gtt cgc cag gct cca gga aaa ggt ctg 143  
 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 35 40 45

gag tgg gta tca gct att ggt acc ggt ggt ggc aca tac tat gca gac 191  
 Glu Trp Val Ser Ala Ile Gly Thr Gly Gly Thr Tyr Tyr Ala Asp  
 50 55 60

tcc gtg cag ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc 239  
 Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser  
 65 70 75

ttg tat ctt caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat 287  
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
 80 85 90 95

tac tgt gca aga tac gac gag ccg ctg acg att tac tgg ttt gac tcc 335  
 Tyr Cys Ala Arg Tyr Asp Glu Pro Leu Thr Ile Tyr Trp Phe Asp Ser  
 100 105 110

tgg ggc caa ggt acc ctg gtc acc gtc tcg agt ggt gga ggc ggt tca 383  
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser  
 115 120 125

ggc gga ggt ggc tct ggc ggt ggc gga tcg gaa att gag ctc aca cag 431  
 Gly Gly Gly Ser Gly Gly Ser Gly Ser Glu Ile Glu Leu Thr Gln  
 130 135 140

tct cca gcc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc tcc 479  
 Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser  
 145 150 155

tgc agg gcc agt cag agt gtt agc agc tac tta gcc tgg tac caa cag 527  
 Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln  
 160 165 170 175

aaa cct ggc cag gct ccc agg ctc ctc atc tat gat gca tcc aac agg 575  
 Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg  
 180 185 190

gcc act ggc atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gac 623  
 Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 195 200 205

ttc act ctc acc atc agc agc cta gag cct gaa gat ttt gca gtt tat 671  
 Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr  
 210 215 220

tac tgt cag cag cgt agc aac tgg cct ccg gct ttc ggc gga ggg acc 719  
 Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr  
 225 230 235

aag gtg gag atc aaa cgt gcg gcc gc 745  
 Lys Val Glu Ile Lys Arg Ala Ala  
 240 245

<210> 14  
<211> 247  
<212> PRT  
<213> Artificial sequence

&lt;220&gt;

&lt;223&gt; scFv SC02022

&lt;400&gt; 14

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro  
1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser  
20 25 30

Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Val Ser Ala Ile Gly Thr Gly Gly Thr Tyr Tyr Ala Asp Ser  
50 55 60

Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu  
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr  
85 90 95

Cys Ala Arg Tyr Asp Glu Pro Leu Thr Ile Tyr Trp Phe Asp Ser Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly  
115 120 125

Gly Gly Gly Ser Gly Gly Ser Glu Ile Glu Leu Thr Gln Ser  
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys  
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys  
165 170 175

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala  
180 185 190

Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe  
195 200 205

Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr  
 210 215 220

Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr Lys  
 225 230 235 240

Val Glu Ile Lys Arg Ala Ala  
 245

<210> 15

<211> 745

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02023

<220>

<221> CDS

<222> (3)..(743)

<223>

<400> 15

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1 5 10 15	

cct ggg ggg tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc	95
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe	
20 25 30	

agt agc tat gct atg cac tgg gtt cgc cag gct cca gga aaa ggt ctg	143
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
35 40 45	

gag tgg gta tca gct att ggt act ggt ggc aca tac tat gca gac	191
Glu Trp Val Ser Ala Ile Gly Thr Gly Gly Thr Tyr Tyr Ala Asp	
50 55 60	

tcc gtg atg ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg	239
Ser Val Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr	
65 70 75	

ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat	287
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr	
80 85 90 95	

tac tgt gca aga tac gac aat gtg atg ggt ctt tac tgg ttt gac tac	335
Tyr Cys Ala Arg Tyr Asp Asn Val Met Gly Leu Tyr Trp Phe Asp Tyr	
100 105 110	

tgg ggc caa ggt acc ctg gtc acc gtc tcg agt ggt gga ggc ggt tca	383
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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser			
115	120	125	
ggc gga ggt ggc tct ggc ggt ggc gga tcg gaa att gag ctc aca cag		431	
Gly Gly Gly Ser Gly Gly Ser Gly Glu Ile Glu Leu Thr Gln			
130	135	140	
tct cca gcc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc tcc		479	
Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser			
145	150	155	
tgc agg gcc agt cag agt gtt agc agc tac tta gcc tgg tac caa cag		527	
Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln			
160	165	170	175
aaa cct ggc cag gct ccc agg ctc ctc atc tat gat gca tcc aac agg		575	
Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg			
180	185	190	
gcc act ggc atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gac		623	
Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp			
195	200	205	
ttc act ctc acc atc agc agc cta gag cct gaa gat ttt gca gtt tat		671	
Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr			
210	215	220	
tac tgt cag cag cgt agc aac tgg cct ccg gct ttc ggc gga ggg acc		719	
Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Thr			
225	230	235	
aag gtg gag atc aaa cgt gcg gcc gc		745	
Lys Val Glu Ile Lys Arg Ala Ala			
240	245		
<210> 16			
<211> 247			
<212> PRT			
<213> Artificial sequence			
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<400> 16			
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro			
1 5 10 15			
Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser			
20 25 30			
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu			
35 40 45			
Trp Val Ser Ala Ile Gly Thr Gly Gly Thr Tyr Tyr Ala Asp Ser			
50 55 60			

Val Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu  
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr  
85 90 95

Cys Ala Arg Tyr Asp Asn Val Met Gly Leu Tyr Trp Phe Asp Tyr Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly  
115 120 125

Gly Gly Gly Ser Gly Gly Ser Glu Ile Glu Leu Thr Gln Ser  
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys  
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys  
165 170 175

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala  
180 185 190

Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe  
195 200 205

Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr  
210 215 220

Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr Lys  
225 230 235 240

Val Glu Ile Lys Arg Ala Ala  
245

<210> 17

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02008

<400> 17

Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp Tyr  
1 5 10

<210> 18  
<211> 12  
<212> PRT  
<213> Artificial sequence

<220>  
<223> CDR3 of scFv SC02009  
<400> 18

Asp Arg Tyr Val Asn Thr Ser Asn Ala Phe Asp Tyr  
1 5 10

<210> 19  
<211> 10  
<212> PRT  
<213> Artificial sequence

<220>  
<223> CDR3 of scFv SC02010  
<400> 19

Asp Met Ser Gly Phe His Glu Phe Asp Tyr  
1 5 10

<210> 20  
<211> 12  
<212> PRT  
<213> Artificial sequence

<220>  
<223> CDR3 of scFv SC02011  
<400> 20

Asp Arg Tyr Phe Arg Gln Gln Asn Ala Phe Asp Tyr  
1 5 10

<210> 21  
<211> 10  
<212> PRT  
<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02012

<400> 21

Ala Arg Ala Ala Gly Thr Ile Phe Asp Tyr  
1 5 10

<210> 22

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02021

<400> 22

Asp Arg Tyr Ile Thr Leu Pro Asn Ala Leu Asp Tyr  
1 5 10

<210> 23

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02022

<400> 23

Tyr Asp Glu Pro Leu Thr Ile Tyr Trp Phe Asp Ser  
1 5 10

<210> 24

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02023

<400> 24

Tyr Asp Asn Val Met Gly Leu Tyr Trp Phe Asp Tyr  
1 5 10

<210> 25

<211> 451

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of heavy chain of 008

<400> 25

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr  
20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys  
 210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 435 440 445

Pro Gly Lys  
 450

<210> 26

<211> 449

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of heavy chain of 011

<400> 26

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr  
20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly  
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln  
65 70 75 80

Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
85 90 95

Asp Arg Tyr Phe Arg Gln Gln Asn Ala Phe Asp Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu  
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys  
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro  
 225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
 245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp  
 260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val  
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
 340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr  
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu  
 370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu  
 385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys  
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
 435 440 445

Lys

<210> 27

<211> 451

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Amino acid sequence of heavy chain 021

&lt;400&gt; 27

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Arg	Gly
1					5				10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
					20				25				30		

Ala	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
					35			40					45		

Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
					50			55				60			

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
					65			70			75			80	

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
					85			90					95		

Ala	Lys	Asp	Arg	Tyr	Ile	Thr	Leu	Pro	Asn	Ala	Leu	Asp	Tyr	Trp	Gly
					100			105					110		

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
					115			120				125			

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
					130			135			140				

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
					145			150			155			160	

Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
					165			170			175				

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
					180			185				190			

Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
					195			200				205			

Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys
					210			215			220				

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 435 440 445

Pro Gly Lys  
 450

<210> 28

<211> 450

<212> PRT

<213> Artificial sequence

&lt;220&gt;

&lt;223&gt; Amino acid sequence of heavy chain of 023

&lt;400&gt; 28

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	His	Pro	Gly	Gly
1					5					10				15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
								20	25				30		

Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
								35	40			45			

Ser	Ala	Ile	Gly	Thr	Gly	Gly	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Met	
							50	55		60					

Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu
65							70			75			80		

Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
							85		90				95		

Arg	Tyr	Asp	Asn	Val	Met	Gly	Leu	Tyr	Trp	Phe	Asp	Tyr	Trp	Gly	Gln
					100			105				110			

Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
						115		120			125				

Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
							130	135		140					

Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150				155			160			

Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
						165		170			175				

Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
							180		185		190				

Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
						195		200			205				

Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp
						210		215			220				

Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly
225						230			235			240			

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg  
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Lys  
450

<210> 29

<211> 219

<212> PRT

<213> Artificial sequence

<220>

&lt;223&gt; Amino acid sequence of light chain of 008

&lt;400&gt; 29

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly  
1 5 10 15Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
20 25 30Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser  
35 40 45Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro  
50 55 60Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr  
85 90 95Tyr Asn His Pro Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105 110Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
115 120 125Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
130 135 140Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
145 150 155 160Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
165 170 175Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
180 185 190Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
195 200 205Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

&lt;210&gt; 30

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Amino acid sequence of light chain of 011

&lt;400&gt; 30

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly  
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser  
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr  
85 90 95

Tyr Asn His Pro Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215

&lt;210&gt; 31

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Amino acid sequence of light chain of 021

&lt;400&gt; 31

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Val	Ser	Leu	Pro	Val	Thr	Pro	Gly
1			5					10					15		

Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser
20					25								30		

Asn	Gly	Tyr	Asn	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
35					40						45				

Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg	Ala	Ser	Gly	Val	Pro
50					55					60					

Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65				70					75				80		

Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr
85					90							95			

Lys	Ser	Asn	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys
100					105					110					

Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
115					120						125				

Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
130				135						140					

Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
145					150				155				160		

Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
165					170					175					

Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
180					185					190					

Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
195				200						205					

Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
210					215										

<210> 32

<211> 214

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of light chain of 023

<400> 32

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro  
85 90 95

Ala Phe Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 33  
<211> 55  
<212> DNA  
<213> Artificial sequence

<220>  
<223> 5' cloning site of pPicZalphaB  
<220>  
<221> CDS  
<222> (1)..(54)  
<223>

<400> 33  
tct ctc gag aaa aga gag gct gaa gct gca gga att cac gtg gcc cag 48  
Ser Leu Glu Lys Arg Glu Ala Glu Ala Ala Gly Ile His Val Ala Gln  
1 5 10 15  
ccg gcc g 55  
Pro Ala

<210> 34  
<211> 18  
<212> PRT  
<213> Artificial sequence

<220>  
<223> 5' cloning site of pPicZalphaB  
<400> 34  
Ser Leu Glu Lys Arg Glu Ala Glu Ala Ala Gly Ile His Val Ala Gln  
1 5 10 15  
Pro Ala

<210> 35  
<211> 55  
<212> DNA

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZFH

<220>

<221> CDS

<222> (1)..(54)

<223>

<400> 35

tct ctc gag aaa aga gcc atg gaa gct gca gga att cac gtg gcc cag 48  
Ser Leu Glu Lys Arg Ala Met Glu Ala Ala Gly Ile His Val Ala Gln  
1 5 10 15

ccg gcc g 55  
Pro Ala

<210> 36

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZFH

<400> 36

Ser Leu Glu Lys Arg Ala Met Glu Ala Ala Gly Ile His Val Ala Gln  
1 5 10 15

Pro Ala

<210> 37

<211> 92

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic hinge region

<220>

&lt;221&gt; CDS

&lt;222&gt; (1)...(90)

&lt;223&gt;

&lt;400&gt; 37

gcf gcc gcg cca aag cca agt acc cca cca ggt tct tca tgt cca cca	48
Ala Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Cys Pro Pro	
1 5 10 15	

tgt cca ggc tct ggc ggt gcf cca atc gat agc ggc ttt cta ga	92
Cys Pro Gly Ser Gly Gly Ala Pro Ile Asp Ser Gly Phe Leu	
20 25 30	

&lt;210&gt; 38

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Synthetic hinge region

&lt;400&gt; 38

Ala Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Cys Pro Pro	
1 5 10 15	

Cys Pro Gly Ser Gly Gly Ala Pro Ile Asp Ser Gly Phe Leu	
20 25 30	

&lt;210&gt; 39

&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Nucleotide sequence of heavy chain of 008

<400> 39	
atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtcttga attctccatg	60
gccgagggtgc agctgggtgga gtctggggga ggcttggtcc agcctggagg gtccctgaga	120
ctctcctgtg cagcctctgg attcaccttt agcaactaca cgatgaactg ggtccgccag	180
gcgcggggga aggggctgga gtgggtctca gctattagtg gtatgtggg tagcacatac	240
tacgcagact ccgtgaaggg ccggttcacc atctccagag acaattccaa gaacacgctg	300
tatctgcaaa tgaacagcct gagagccgag gacacggccg tgtattactg tgccaaagac	360

cgctactccc	aggtgtcacta	cgcgttggat	tactggggcc	agggcaccct	ggtgaccgtc	420
tcctcagcct	ccaccaaggg	cccatcggtc	ttccccctgg	caccctcctc	caagagcacc	480
tctggggca	cagcggccct	gggctgcctg	gtcaaggact	acttccccga	accggtgacg	540
gtgtcggtga	actcaggcgc	cctgaccagc	ggcgtgcaca	ccttccggc	tgtcctacag	600
tcctcaggac	tctactccct	cagcagcgtg	gtgaccgtgc	cctccagcag	cttgggcacc	660
cagacctaca	tctgcaacgt	gaatcacaag	cccagcaaca	ccaagggtga	caagagagtt	720
gagcccaaat	cttgtgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaactcctg	780
gggggaccgt	cagtcttcct	cttccccca	aaacccaagg	acaccctcat	gatctccgg	840
acccctgagg	tcacatgcgt	ggtgggtggac	gtgagccacg	aagaccctga	ggtcaagttc	900
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	960
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	1020
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	cagccccat	cgagaaaacc	1080
atctccaaag	ccaaaggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccg	1140
gaggagatga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatcccagc	1200
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	1260
cccggtctgg	actccgacgg	ctccttcttc	ctctatagca	agtcaccgt	ggacaagagc	1320
aggtggcagc	aggggaacgt	cttctcatgc	tccgtatgc	atgaggctct	gcacaaccac	1380
tacacgcaga	agagcctctc	cctgtctccg	ggtaaa			1416

&lt;210&gt; 40

&lt;211&gt; 1410

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Nucleotide sequence of heavy chain of 011

&lt;400&gt; 40

atggcatgcc	ctggcttcct	gtgggcactt	gtgatctcca	cctgtcttga	attctccatg	60
gccgagggtgc	agctggtgga	gtctggggga	ggcgtggtcc	agcctggag	gtccctgaga	120
ctctcctgtg	cagcctctgg	attcaccttc	agcgactaca	cgtgaactg	ggtccgccag	180
gcgccccggga	aggggctgga	gtgggtctca	tccatttagt	gtggtagcac	atactacgca	240
gactccagga	agggcagatt	caccatctcc	agagacaatt	ccaaagaacac	gctgtatctt	300
caaatagaaca	acctgagagc	tgaggacacg	gccgtgtatt	actgtgcaag	agaccgctac	360
ttcaggcagc	agaacgcgtt	cgattactgg	ggccaggca	ccctggtgac	cgtctccctca	420
gcctccacca	agggcccatc	ggtctccccc	ctggcaccct	cctccaagag	cacctctggg	480

ggcacagcgg	ccctgggctg	cctggtaaag	gactacttcc	ccgaaccgg	gacggtgtcg	540
tggaaactca	gcccctgac	cagcggcgtg	cacaccc	cgctgtcct	acagtcc	600
ggactctact	ccctcagcag	cgtggt	gacc	gtgc	cctcca	660
tacatctgca	acgtgaatca	caagccc	aacccaagg	tggaca	agag	720
aaatctt	gtg	acatca	cacatgccc	ccgt	gccc	780
ccgtcag	tcctt	ccc	aaaaaccc	aagg	acac	840
gaggtc	acat	gcgtgg	gggt	ggacgt	gagc	900
tacgtgg	gacg	gcgtgg	gaggt	gcataat	gccc	960
agcacgt	acc	gtgtgg	tca	gtat	gtc	1020
gagtaca	agt	gcaagg	tctc	ccat	gcacc	1080
aaagccaa	ag	ggcag	cccc	agaacc	acag	1140
atgacca	aga	accagg	tcag	cctgac	ctgg	1200
gccgtgg	agt	gggag	gagcaa	tggcag	cccg	1260
ctggact	ccg	ggc	ccct	ttc	ctat	1320
cagcagg	gg	acgt	ttt	atgct	ccgt	1380
cagaag	ag	atg	ccgt	atgc	atgg	1410

&lt;210&gt; 41

&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Nucleotide sequence of heavy chain of 021

&lt;400&gt; 41

atggcat	cc	ctggctt	cct	gtggc	actt	gtgat	cttcca	cctgt	tgt	att	ctccat	60
gccgagg	tg	tc	gt	gg	gg	gt	ctgg	gt	tt	tt	ccat	120
ctctc	c	c	c	c	c	c	c	c	c	c	c	180
gcgc	cc	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	240
tacgc	ag	ac	gg	gg	gg	gg	gg	gg	gg	gg	gg	300
tatct	g	ca	aa	gg	cc	tt	cc	cc	cc	cc	cc	360
cgct	ac	at	ca	cc	tt	cc	cc	cc	cc	cc	cc	420
tcct	c	ac	at	cc	gg	cc	cc	cc	cc	cc	cc	480
tct	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	540
gtgt	cgt	gg	ga	gg	cc	cc	cc	cc	cc	cc	cc	600

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt	720
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	780
gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctccgg	840
acccctgagg tcacatgcgt ggtggtgac gtgagccacg aagaccctga ggtcaagttc	900
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgacg ggaggagcag	960
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgaccaggaa ctggctgaat	1020
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc	1080
atctccaaag ccaaaggca gccccgagaa ccacaggtgt acaccctgcc cccatccgg	1140
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1260
cccggtctgg actccgacgg ctccttcttc ctctatagca agtcaccgt ggacaagagc	1320
aggtggcagc agggaaacgt cttctcatgc tccgtatgc atgaggctct gcacaaccac	1380
tacacgcaga agaccctctc cctgtctccg ggtaaa	1416

<210> 42

<211> 1413

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of heavy chain of 023

<400> 42	
atggcatgcc ctggcttcct gtggcactt gtgatctcca cctgtcttga attctccatg	60
gccgagggtgc agctggtgga gtctggggga ggctgggtac atcctggggg gtccctgaga	120
ctctcctgtg caggctctgg attcaccttc agtagctatg ctatgcactg ggtcgcacg	180
gctccaggaa aaggctctgga gtgggtatca gctattggta ctgggtggc cacatactat	240
gcagactccg tcatggcccg gttcaccatc tccagagaca attccaagaa cacgctgtat	300
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc aagatacgcac	360
aatgtgatgg gtcttactg gttgactac tggggccagg gcaccctggt gaccgtctcc	420
tcagcctcca ccaagggccc atcggcttcc cccctggcac cctcctccaa gacgcacctct	480
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	540
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc	600
tcaggactct actccctcag cagcgtggtg accgtccct ccagcagctt gggcacccag	660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag	720

cccaaatctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	780
ggaccgtca	gtttcccttt	ccccccaaaa	cccaaggaca	ccctcatgat	ctcccgacc	840
cctgagggtca	catgcgtgg	gttggacgtg	agccacgaag	accctgaggt	caagttcaac	900
tggtacgtgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	960
aacagcacgt	accgtgtgg	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	1020
aaggagtaca	agtgc当地	ctccaacaaa	gccc当地	cccccatcga	gaaaaccatc	1080
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atccc当地	1140
gagatgacca	agaaccaggt	cagcctgacc	tgc当地	aaggcttcta	tccc当地	1200
atcgccgtgg	agtggagag	caatggcag	ccggagaaca	actacaagac	cacgc当地	1260
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1320
tggcagcagg	gaaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1380
acgcagaaga	gcctctccct	gtctccgggt	aaa			1413

&lt;210&gt; 43

&lt;211&gt; 720

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Nucleotide sequence of light chain of 008

<400> 43	atggcatgcc	ctggcttcct	gtgggcactt	gtgatctcca	cctgtctcga	gtttccatg	60
	gctgacatcg	tatgacaca	gtctccagac	tcactgccc	tcacccctgg	agagccggcc	120
	tccatctcct	gcaggtctag	ttaggcctc	ctgcatagta	atggatacaa	ctatttggat	180
	tggtacctgc	agaaggcagg	gcagtctcca	cagctcctga	tctatgggg	ttctaatcgg	240
	gcctccgggg	tccctgacag	gttcagtgcc	agtggatcag	gcacagat	tacactgaaa	300
	atcagcagag	tggaggctga	gatgttggg	gtttattact	gccagcagta	ctacaaccac	360
	ccgacgac	tcggccaggg	caccaaactg	gaaatcaa	gtactgtggc	tgcaccatct	420
	gtcttcatct	tcccccattc	tatgagcag	ttgaaatctg	gaactgcctc	tgttgtgc	480
	ctgctgaata	acttctatcc	cagagaggcc	aaagtacagt	ggaagggtgga	taacgc当地	540
	caatcgggta	actcccagga	gagtgtcaca	gagcaggaca	gcaaggacag	cacctacagc	600
	ctcagcagca	ccctgacgct	gagcaaagca	gactacgaga	aacacaaa	gtacgc当地	660
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<212> DNA

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<223> Nucleotide sequence of light chain of 011

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<211> 720

<212> DNA

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<223> Nucleotide sequence of light chain of 021

<400> 45

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ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc	660
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<212> DNA

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<223> Primer

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<211> 49

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<223> Primer

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49

<210> 50

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